

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:28 ; Search time 8498.8 seconds
(without alignments)
31.610 Million cell updates/sec

Title: US-09-851-670-17

Perfect score: 25

Sequence: 1 ctccacttggaatcaccgtacaca 25

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 segs, 537289281 residues

Total number of hits satisfying chosen parameters: 111874

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estom:*
5: em_estopl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rnd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.6	58.4	49	13	PCH303694
C 2	14.2	56.8	39	13	A2663277
C 3	14	56.0	27	13	A2477331
C 4	14	56.0	53	10	AA833683
C 5	13.8	55.2	43	10	A1020738
C 6	13.8	55.2	53	13	TA129A090
C 7	13.6	54.4	52	11	BF631900
C 8	13.4	53.6	52	10	AA394031
C 9	13.4	53.6	60	11	D43017
C 10	13	52.0	50	10	AU107342
C 11	13	52.0	54	10	AA194224
C 12	12.8	51.2	41	11	D25852

C 13	12.6	50.4	46	11	T73147
C 14	12.6	50.4	47	11	R52627
C 15	12.6	50.4	55	10	AA038583
C 16	12.4	49.6	34	13	A2587290
C 17	12.4	49.6	41	10	AA683660
C 18	12.4	49.6	49	10	AA933986
C 19	12.4	49.6	52	10	AA702879
C 20	12.4	49.6	52	10	AA184887
C 21	12.4	49.6	53	10	AA654368
C 22	12.4	49.6	53	10	AA431961
C 23	12.4	49.6	53	10	AA484556
C 24	12.4	49.6	53	10	AA542866
C 25	12.4	49.6	53	10	AA557718
C 26	12.4	49.6	53	10	AA568432
C 27	12.4	49.6	53	10	AA583175
C 28	12.4	49.6	53	10	AA625891
C 29	12.4	49.6	53	13	A2576214
C 30	12.2	48.0	59	13	A2848297
C 31	12	48.0	47	13	A2657746
C 32	12	48.0	50	13	TA19A060
C 33	11.8	47.2	39	13	A2784783
C 34	11.8	47.2	43	10	AA906764
C 35	11.8	47.2	43	13	A2591374
C 36	11.8	47.2	45	13	A2761741
C 37	11.8	47.2	46	10	AA972734
C 38	11.8	47.2	47	10	AA857783
C 39	11.8	47.2	49	13	CNS074TU
C 40	11.8	47.2	50	10	AU102680
C 41	11.8	47.2	52	10	AA565659
C 42	11.8	47.2	52	11	BF634385
C 43	11.8	47.2	53	10	A1027736
C 44	11.8	47.2	54	10	AA630207
C 45	11.8	47.2	54	13	A2818750

ALIGNMENTS

RESULT 1
LOCUS PCH303694 49 bp DNA GSS 03-APR-2001
DEFINITION Plasmodium chabaudi genome survey sequence, clone PC9H11.plt.
ACCESSION AJ303694
VERSION AJ303694.1 GI:11140201
KEYWORDS GSS: genome survey sequence.
SOURCE Plasmodium chabaudi.
ORGANISM Plasmodium chabaudi
REFERENCE
AUTHORS Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,
Bowman,S., Phillips,R.S. and Turner,C.M.
TITLE Gene discovery in Plasmodium chabaudi by genome survey sequencing
JOURNAL Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
MEDLINE 21192558
REFERENCE 2 (bases 1 to 49)
AUTHORS Janssen,C.S.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2000) Division of Infection & Immunity,
University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
COMMENT bases 122 to 170 (OL to OR).
FEATURES
source
1..49
/organism="Plasmodium chabaudi"
/db_xref="taxon:5825"
/clone="PC9H11.plt"
BASE COUNT 9 a 11 c 10 g 19 t
ORIGIN
Query Match 58.4% Score 14.6; DB 13; Length 49;
Best Local Similarity 81.0% Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY      4 caacttgaatcacgylacac 24
         ||| || ||||| |||||
Db      48 CAGCTCGGAATCAGAGTACAC 28
```

RESULT	2
AZ663277/c	
LOCUS	AZ663277 39 bp DNA 14-DEC-2000
DEFINITION	M05054017 Mouse 10kb plasmid UUC1M library Mus musculus genomic
ACCESSION	AZ663277
VERSION	AZ663277
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
1 (bases 1 to 39)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: ddumegenetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0542 row: 0 column: 15
 Seq primer: CACACAGGAAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 39.
 Location/Qualifiers
 1..39

```

SOURCE
1. 39
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="U061M0542015"
/clone_id="Mouse 10kb plasmid U061M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42uv: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1147321149b1A129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match	Score	DB	Length
56.88;	14.2;	13;	39;
Best Local Similarity	84.28;	Pred. No. 1.6e+04;	

	Matches	16, Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	5	aacttggaatcacgtaca	23						
Db	32	AACTTAATAATCACGGAACA	14						

RESULT	3
AZ477331	
LOCUS	AZ477331 27 bp DNA GSS
DEFINITION	IM0296G1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION	AZ477331
VERSION	AZ477331
KEYWORDS	Clone UUGC1M0296G14 R. DNA sequence.
SOURCE	AZ477331.1 GI:10635544
ORGANISM	GSS. house mouse. Mus musculus.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 27)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Stokes, R., Tinger, A., von Niederhausern, A. and Wright, D. Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10xb	Plasmid inserts	
	Unpublished (2000)			Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0296 row: G column: 14
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

SOURCE

Location/Qualifiers

1. 27

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0296G14"

/clone_1bp="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD12 (g114732114[9b]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into. Chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

9 a 6 c 5 g 7 t

BRIGIN

Query Match 56.08; Score 14; DB 13; Length 27;

ACCESSION	AL463861
VERSION	AL463861.1
KEYWORDS	GI:11834186
SOURCE	GSS.
ORGANISM	Trypanosoma brucei. Trypanosoma brucei Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE	1 (bases 1 to 53)
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Meyville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).
FEATURES	Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/ Location/Qualifiers
source	1..53 /organism="Trypanosoma brucei" /strain="TREU927" /db_xref="taxon:5691" /clone="129a09"
BASE COUNT	16 a 13 c 9 g 15 t
ORIGIN	
Query Match	55.2%; Score 13.8; DB 13; Length 53; Best Local Similarity 72.0%; Pred. No. 2.5e+04;
Matches	18; Conservative 0; Mismatches 7; Indels 0; Gaps 0
Oy	1 ctccaacttggaatacaggtacaca 25
Dd	44 CACCGAGTTGCATTCACGCTAAAAA 20
RESULT 7	
LOCUS	BFG31900 52 bp mRNA EST 19-DEC-2000
DEFINITION	NF016F05DRI1044 Drought Medicago truncatula cDNA clone NF016F05DT
ACCESSION	BFG31900
VERSION	BFG31900
KEYWORDS	BFG31900.1 GI:11896058
SOURCE	EST.
ORGANISM	bareil medic. Medicago truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoidae; Trifolieae Medicago.
REFERENCE	1 (bases 1 to 52)
AUTHORS	Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
JOURNAL	Unpublished (2000)
COMMENT	Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380

```

Email: gdmay@noble.org
Insert Length: 52 Std Error: 0.00
Plate: 016 Row: F Column: 05
Seq primer: TCACACAGGAACACAGCTATGAC.
FEATURES
    source
        1..52
            /organism="Medicago truncatula"
            /db_xref="taxon:3880"
            /clone="NF016F05DP"
            /clone_lib="Drought"
            /tissue_type="Plantlets"
            /dev_stage="Pooled timepoints"
            /note="Vector: lambda zap; Contains a mixture of entire
            plantlets harvested in a series of days-post-watering
            timepoints."
BASE COUNT      21 a      17 c      3 g      11 t
ORIGIN
Query Match      54.4%; Score 13.6; DB 11; Length 52;
Best Local Similarity 80.0%; Pred. No. 3,1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy      6 acttgaatcacggtacaca 25
        ||||| || || || |||||
        10 ACTTCACACAGACGCTACACA 29
RESULT      8
AA394031/c
LOCUS
DEFINITION
        AA394031      52 bp      mRNA
        zt55ell.r1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:729164
        5' similar to WP:DI022.1 CE02575 UBIQUITIN-CONJUGATING ENZYME ;
        mRNA sequence.
        AA394031
        AA394031.1 GI:2047018
        EST.
        human.
SOURCE
    ORGANISM
        Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
        1 (bases 1 to 52)
        Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geiscl, G., Jost, S.,
        Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
        Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie
        , T., Waterston, R., and Wilson, R.
        Washu-Merck EST Project 1997
        Unpublished (1997)
        Contact: Wilson RK
        Washington University School of Medicine
        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
        Tel: 314 286 1800
        Fax: 314 286 1810
        Email: est@watson.wustl.edu
        This clone is available royalty-free through LNL; contact the
        IMAGE Consortium (info@image.lnl.gov) for further information.
        Trace considered overall poor quality
        Possible reversed clone: similarity on wrong strand
        Seq primer: -28ml3 rev2 ET from Amer sham
        High quality sequence stop: 1.
        Location/Qualifiers
            1..52
                /organism="Homo sapiens"
                /db_xref="GDB:592563"
                /db_xref="taxon:9606"
                /clone="IMAGE:729164"
                /clone_lib="Soares_tests_NHT"
                /sex="Male"
                /lab_host="DH10B"
                /note="Vector: pUT73D-Pac (Pharmacia) with a modified
                polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                was prepared from mRNA obtained from Clontech Laboratories
                , Inc., and primed with a Not I - oligo(dT) primer [5'

```

TCCTACCAATCTGAAGTGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 12 a 9 c 19 g 12 t

ORIGIN

Query Match 53.6%; Score 13.4; DB 10; Length 52;
 Best Local Similarity 73.9%; Pred. No. 3.8e+04;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 2 tccaacttggaatcacggtacac 24
 Db 33 TCAAACTCGAGTCTCGGTCC 11

RESULT 9
 DA3017/c 60 bp mRNA EST 04-MAY-1998

LOCUS D43017 Rice callus cDNA (H.Uchimiya) Oryza sativa cDNA clone AD344,
 DEFINITION mRNA sequence.

ACCESSION D43017
 VERSION D43017.1 GI:3107277

KEYWORDS EST.
 SOURCE Oryza sativa.

ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.

REFERENCE 1 (bases 1 to 60)

AUTHORS Uchimiya,H.

TITLE On nucleotide sequence of Oryza sativa

JOURNAL Unpublished (1994)

COMMENT Contact: Hirofumi Uchimiya
 Institute of Mol. & Cell. Bioscience, Department of Cellular

Function

The University of Tokyo

1-1-1 Yayoi, Bunkyo-ku, Tokyo 113, Japan

Tel: 03-3812-2111(ex.7844)

Fax: 03-3812-2910

Email: huchimiya@ansel.cc.u-tokyo.ac.jp

PROJECT= uchimiya

FEATURES Location/Qualifiers

source

1..60

/organism="Oryza sativa"

/db_xref="taxon:4530"

/clone="AD344"

/issue_type="Rice callus cDNA (H.Uchimiya)"

/issue_type="callus"

BASE COUNT 12 a 20 c 15 g 11 t

ORIGIN

Query Match 53.6%; Score 13.4; DB 11; Length 60;

Best Local Similarity 73.9%; Pred. No. 3.9e+04;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ctccaacttggaatcacggtacac 23

Db 49 CCCGACTGTAGTACCGGTACA 27

RESULT 10

AU107342

LOCUS AU107342 50 bp mRNA EST

DEFINITION AU107342 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

ADRA02874, mRNA sequence.

ACCESSION AU107342

VERSION AU107342.1 GI:13556863

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata

,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo

,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human

mRNAs using full-length enriched and 5'-end enriched cDNA libraries

Unpublished (2001)

COMMENT Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano

,S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES Location/Qualifiers

source

1..50

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="ADRA02874"

/issue_type="Sugano Homo sapiens cDNA library"

BASE COUNT 10 a 15 c 11 g 14 t

ORIGIN

Query Match 52.0%; Score 13; DB 10; Length 50;
 Best Local Similarity 76.2%; Pred. No. 5.8e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 ctccaacttggaatcacggtacac 21

Db 1 CCCGAAGTGGAGTCTCGGTACA 21

RESULT 11

AA194224

LOCUS AA194224 54 bp mRNA EST 12-MAR-1998

DEFINITION zq04c04.r1 Stragatene muscle 937209 Homo sapiens cDNA clone

IMAGE:628710 5' similar to gb:M73628 KAPPA CASEIN PRECURSOR (HUMAN

);, mRNA sequence.

ACCESSION AA194224

VERSION AA194224.1 GI:1784116

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 54)

AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin

,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,

White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project

Unpublished (1997)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LML; contact the

IMAG Consortium (info@image.llnl.gov) for further information.

Insert length: 819 Std Error: 0.00

High quality sequence stop: 1.

FEATURES Location/Qualifiers

source

1..54

/organism="Homo sapiens"

/db_xref="GDB:5048944"

/db_xref="taxon:9606"

/clone="IMAGE:628710"
/clone_lib="Stratagene muscle 937209"
/issue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally.
Primer: Oligo dT. Skeletal muscle from patient with
malignant hyperthermia. Average insert size: 1.0 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGCGCAGCAG
3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

BASE COUNT
14 a 9 c 9 g 21 t 1 others

ORIGIN

Query Match
Best Local Similarity 52.0%; Score 13; DB 10; Length 54;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 tcccaactggaatcaggtaca 23
18 tcccaactggaatcaggtaca 39

RESULT 12
D25852 41 bp mRNA EST 30-NOV-1995
LOCUS HUMS04228 Human colon mucosa Homo sapiens cDNA clone cm2172 3',
DEFINITION mRNA sequence.
ACCESSION D25852
VERSION D25852.1 GI:500520
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 41)
Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K.
Global analysis of gene expression in colon mucosa: a large scale
random cDNA sequencing analysis
JOURNAL Unpublished (1994)
COMMENT Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K.
Institute for Molecular and Cellular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.
FEATURES
Location/Qualifiers
1..41
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cm2172"
/clone_lib="Human colon mucosa"
/note="Adult male, tissue type = colon mucosa "

BASE COUNT
15 a 8 c 3 g 15 t

ORIGIN

Query Match
Best Local Similarity 51.2%; Score 12.8; DB 11; Length 41;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 ctccaactggaatcaggtacac 24
4 ctccaactggaatcaggtacac 27

RESULT 13
T73147 46 bp mRNA EST 02-MAR-1995
LOCUS T73147/c
DEFINITION yc67e02.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:85754 3' similar to gb:xs4486_mnal PLASMA PROTEASE C1
INHIBITOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION T73147
VERSION T73147.1 GI:689822

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 46)
Hallier, L., Lemmo, G., Becker, M., Bonaldo, M.F., Chappel, B.,
Chissoe, S., Dietrich, N., Dubugue, T., Favell, A., Gish, W., Hawkins
B., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Maris, E., Moore
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, D., Trevisan, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Matis, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
TITLE Contact: Wilson, R.
JOURNAL Washington University School of Medicine
MEDLINE 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
COMMENT Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1353
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNL This clone is available royalty-free
through LNL; contact the IMAGE Consortium (info@image.lnl.gov)
for further information. Trace considered overall poor quality
Insert length: 1353 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..46
/organism="Homo sapiens"
/db_xref="Gene:502811"
/db_xref="taxon:9606"
/clone="IMAGE:85754"
/clone_lib="Stratagene liver (#937224)"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'
GAATTCGCGCAGCAG 3' -3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTT 3' "

BASE COUNT
15 a 12 c 11 g 7 t 1 others

ORIGIN

Query Match
Best Local Similarity 50.4%; Score 12.6; DB 11; Length 46;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ctccaactggaatcaggt 20
28 ctccaactggaatcaggt 9

RESULT 14
R52627 47 bp mRNA EST 18-MAY-1995
LOCUS R52627
DEFINITION yg82c02.s1 Soares infant brain INTB Homo sapiens cDNA clone
IMAGE:39999 3' similar to gb:U13710|HUMSCALIN Human scRNA molecule,
transcribed from Aliu (rRNA); gb:M62424 THROMBIN RECEPTOR PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION R52627
VERSION R52627.1 GI:814529
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 47)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.
The WashU-Merck EST Project

JOURNAL COMMENT

Unpublished (1995)
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality
Insert Length: 1970 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1.47
/organism="Homo sapiens"
/db_xref="GDB:412540"
/db_xref="taxon:9606"
/clone="IMAGE:39999"
/clone_lib="Soares infant brain INTB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lactaid BA; Site: 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGCGCGCCGACGACATTTTGTGTGTGT 3'];
double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lactaid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 7 a 10 c 17 g 10 t 3 others
ORIGIN

Query Match 50.4%; Score 12.6; DB 11; Length 47;
Best Local Similarity 71.4%; Pred. No. 8.7e+04;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 ctccactcgtgaatcacggtta 21
||| | ||||| |||||
Db 9 CTCANCGNCTATATCCCGGTA 29

RESULT 15
AA038583 55 bp mRNA EST 28-AUG-1996
LOCUS m185d11.r1 Soares mouse p3NM19.5 Mus musculus cDNA clone
DEFINITION IMAGE:473397 5' similar to SW:KTH_HUMAN P23919 THYMIDYLATE KINASE
; mRNA sequence.

ACCESSION AA038583
VERSION AA038583.1 GI:1513989
KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:284141

Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1.55
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:473397"
/clone_lib="Soares mouse p3NM19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TCTTCCATCTGAGTGGAGCGCGCGCATTTTGTGTGTGT 3'];
double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
BASE COUNT 9 a 13 c 23 g 10 t
ORIGIN

Query Match 50.4%; Score 12.6; DB 10; Length 55;
Best Local Similarity 78.9%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 ctgtgaatcacgttacaca 25
||| | ||||| |||||
Db 43 CTGCGACGACGCGTCCACA 25

Search completed: March 9, 2002, 00:09:30
Job time: 11046 sec

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